



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/808,121A

DATE: 08/06/2004

TIME: 14:27:47

Input Set : D:\V9661069.app

Output Set: N:\CRF4\08062004\J808121A.raw

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3 <110> APPLICANT: PEIRIS, JOSEPH S. M.
4     YUEN, KWOK YUNG
5     POON, LIT MAN
6     GUAN, YI
7     CHAN, KWOK HUNG
8     NICHOLLS, JOHN
10 <120> TITLE OF INVENTION: NOVEL HUMAN VIRUS CAUSING SEVERE ACUTE RESPIRATORY SYNDROME
11     (SARS) AND USES THEREOF
13 <130> FILE REFERENCE: V9661.0069
15 <140> CURRENT APPLICATION NUMBER: 10/808,121A
16 <141> CURRENT FILING DATE: 2004-03-24
18 <150> PRIOR APPLICATION NUMBER: 60/457,031
19 <151> PRIOR FILING DATE: 2003-03-24
21 <150> PRIOR APPLICATION NUMBER: 60/457,730
22 <151> PRIOR FILING DATE: 2003-03-26
24 <150> PRIOR APPLICATION NUMBER: 60/459,931
25 <151> PRIOR FILING DATE: 2003-04-02
27 <150> PRIOR APPLICATION NUMBER: 60/460,357
28 <151> PRIOR FILING DATE: 2003-04-03
30 <150> PRIOR APPLICATION NUMBER: 60/461,265
31 <151> PRIOR FILING DATE: 2003-04-08
33 <150> PRIOR APPLICATION NUMBER: 60/464,886
34 <151> PRIOR FILING DATE: 2003-04-23
36 <160> NUMBER OF SEQ ID NOS: 2470
38 <170> SOFTWARE: PatentIn ver. 3.2
40 <210> SEQ ID NO: 1
41 <211> LENGTH: 646
42 <212> TYPE: DNA
43 <213> ORGANISM: Human severe acute respiratory syndrome virus
45 <220> FEATURE:
46 <221> NAME/KEY: CDS
47 <222> LOCATION: (2)...(646)
49 <400> SEQUENCE: 1
50 a cag gac gct gta gct tca aaa atc tta gga ttg cct acg cag act gtt 49
51   Gln Asp Ala Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val
52     1             5             10             15
54 gat tca tca cag ggt tct gaa tat gac tat gtc ata ttc aca caa act   97
55 Asp Ser Ser Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln Thr
56           20             25             30
58 act gaa aca gca cac tct tgt aat gtc aac cgc ttc aat gtg gct atc   145
59 Thr Glu Thr Ala His Ser Cys Asn Val Asn Arg Phe Asn Val Ala Ile
60           35             40             45
62 aca agg gca aaa att ggc att ttg tgc ata atg tct gat aga gat ctt   193

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63 Thr Arg Ala Lys Ile Gly Ile Leu Cys Ile Met Ser Asp Arg Asp Leu
64      50                      55                      60
66 tat gac aaa ctg caa ttt aca agt cta gaa ata cca cgt cgc aat gtg   241
67 Tyr Asp Lys Leu Gln Phe Thr Ser Leu Glu Ile Pro Arg Arg Asn Val
68 65                      70                      75                      80
70 gct acā tta caa gca gaa aat gta act gga ctt ttt aag gac tgt agt   289
71 Ala Thr Leu Gln Ala Glu Asn Val Thr Gly Leu Phe Lys Asp Cys Ser
72                      85                      90                      95
74 aag atc att act ggt ctt cat cct aca cag gca cct aca cac ctc agc   337
75 Lys Ile Ile Thr Gly Leu His Pro Thr Gln Ala Pro Thr His Leu Ser
76      100                      105                      110
78 gtt gat ata aaa ttc aag act gaa gga tta tgt gtt gac ata cca ggc   385
79 Val Asp Ile Lys Phe Lys Thr Glu Gly Leu Cys Val Asp Ile Pro Gly
80      115                      120                      125
82 ata cca aag gac atg acc tac cgt aga ctc atc tct atg atg ggt ttc   433
83 Ile Pro Lys Asp Met Thr Tyr Arg Arg Leu Ile Ser Met Met Gly Phe
84      130                      135                      140
86 aaa atg aat tac caa gtc aat ggt tac cct aat atg ttt atc acc cgc   481
87 Lys Met Asn Tyr Gln Val Asn Gly Tyr Pro Asn Met Phe Ile Thr Arg
88 145                      150                      155                      160
90 gaa gaa gct att cgt cac gtt cgt gcg tgg att ggc ttt gat gta gag   529
91 Glu Glu Ala Ile Arg His Val Arg Ala Trp Ile Gly Phe Asp Val Glu
92                      165                      170                      175
94 ggc tgt cat gca act aga gat gct gtg ggt act aac cta cct ctc cag   577
95 Gly Cys His Ala Thr Arg Asp Ala Val Gly Thr Asn Leu Pro Leu Gln
96      180                      185                      190
98 cta gga ttt tct aca ggt gtt aac tta gta gct gta ccg act ggt tat   625
99 Leu Gly Phe Ser Thr Gly Val Asn Leu Val Ala Val Pro Thr Gly Tyr
100      195                      200                      205
102 gtt gac act gaa aat aac cta   646
103 Val Asp Thr Glu Asn Asn Leu
104      210                      215
107 <210> SEQ ID NO: 2
108 <211> LENGTH: 215
109 <212> TYPE: PRT
110 <213> ORGANISM: Human severe acute respiratory syndrome virus
112 <400> SEQUENCE: 2
113 Gln Asp Ala Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val
114 1                      5                      10                      15
116 Asp Ser Ser Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln Thr
117      20                      25                      30
119 Thr Glu Thr Ala His Ser Cys Asn Val Asn Arg Phe Asn Val Ala Ile
120      35                      40                      45
122 Thr Arg Ala Lys Ile Gly Ile Leu Cys Ile Met Ser Asp Arg Asp Leu
123      50                      55                      60
125 Tyr Asp Lys Leu Gln Phe Thr Ser Leu Glu Ile Pro Arg Arg Asn Val
126 65                      70                      75                      80
128 Ala Thr Leu Gln Ala Glu Asn Val Thr Gly Leu Phe Lys Asp Cys Ser
129      85                      90                      95

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131 Lys Ile Ile Thr Gly Leu His Pro Thr Gln Ala Pro Thr His Leu Ser
132           100           105           110
134 Val Asp Ile Lys Phe Lys Thr Glu Gly Leu Cys Val Asp Ile Pro Gly
135           115           120           125
137 Ile Pro Lys Asp Met Thr Tyr Arg Arg Leu Ile Ser Met Met Gly Phe
138           130           135           140
140 Lys Met Asn Tyr Gln Val Asn Gly Tyr Pro Asn Met Phe Ile Thr Arg
141 145           150           155           160
143 Glu Glu Ala Ile Arg His Val Arg Ala Trp Ile Gly Phe Asp Val Glu
144           165           170           175
146 Gly Cys His Ala Thr Arg Asp Ala Val Gly Thr Asn Leu Pro Leu Gln
147           180           185           190
149 Leu Gly Phe Ser Thr Gly Val Asn Leu Val Ala Val Pro Thr Gly Tyr
150           195           200           205
152 Val Asp Thr Glu Asn Asn Leu
153           210           215
156 <210> SEQ ID NO: 3
157 <211> LENGTH: 17
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: primer sequence for RT-PCT based on partial
163     nucleotide sequence of the genome of hSARS
165 <400> SEQUENCE: 3
166 tacacacctc agcgttg                                     17
168 <210> SEQ ID NO: 4
169 <211> LENGTH: 16
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: primer sequence for RT-PCT based on partial
175     nucleotide sequence of the genome of hSARS
177 <400> SEQUENCE: 4
178 cacgaacgtg acgaat                                     16
180 <210> SEQ ID NO: 5
181 <211> LENGTH: 27
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: degenerated primer in Superscript II Kit by
187     Invitrogen
189 <220> FEATURE:
190 <221> NAME/KEY: misc_feature
191 <222> LOCATION: (21)..(27)
192 <223> OTHER INFORMATION: a, t, c or g
194 <400> SEQUENCE: 5
W--> 195 gccggagctc tgcagaattc nnnnnnnn                                     27
197 <210> SEQ ID NO: 6
198 <211> LENGTH: 20

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199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: primer provided in AmpliTaq Gold Kit by Applied
204     Biosyndromes
206 <400> SEQUENCE: 6
207 gccggagctc tgcagaattc                                20
209 <210> SEQ ID NO: 7
210 <211> LENGTH: 17
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: First round of primer for amplifying human
216     metapneumovirus (HMPV)
218 <400> SEQUENCE: 7
219 aargtsaatg catcagc                                    17
221 <210> SEQ ID NO: 8
222 <211> LENGTH: 20
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: first round primer for amplifying human
228     metapneumovirus (HMPV)
230 <400> SEQUENCE: 8
231 cakattytgc ttatgctttc                                20
233 <210> SEQ ID NO: 9
234 <211> LENGTH: 20
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: nested primer for amplifying human metapneumovirus
240     (HMPV)
242 <400> SEQUENCE: 9
243 acacctgtta caataccagc                                20
245 <210> SEQ ID NO: 10
246 <211> LENGTH: 19
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: nested primer for amplifying human metapneumovirus
252     (HMPV)
254 <400> SEQUENCE: 10
255 gacttgagtc ccagctcca                                    19
257 <210> SEQ ID NO: 11
258 <211> LENGTH: 1213
259 <212> TYPE: DNA
260 <213> ORGANISM: Human severe acute respiratory syndrome virus
262 <220> FEATURE:
263 <221> NAME/KEY: CDS

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Input Set : D:\V9661069.app

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264 <222> LOCATION: (2)...(1213)
266 <400> SEQUENCE: 11
267 t aaa tgt agt aga atc ata cct gcg cgt gcg cgc gta gag tgt ttt gat 49
268   Lys Cys Ser Arg Ile Ile Pro Ala Arg Ala Arg Val Glu Cys Phe Asp
269     1           5           10           15
271 aaa ttc aaa gtg aat tca aca cta gaa cag tat gtt ttc tgc act gta 97
272 Lys Phe Lys Val Asn Ser Thr Leu Glu Gln Tyr Val Phe Cys Thr Val
273           20           25           30
275 aat gca ttg cca gaa aca act gct gac att gta gtc ttt gat gaa atc 145
276 Asn Ala Leu Pro Glu Thr Thr Ala Asp Ile Val Val Phe Asp Glu Ile
277           35           40           45
279 tct atg gct act aat tat gac ttg agt gtt gtc aat gct aga ctt cgt 193
280 Ser Met Ala Thr Asn Tyr Asp Leu Ser Val Val Asn Ala Arg Leu Arg
281           50           55           60
283 gca aaa cac tac gtc tat att ggc gat cct gct caa tta cca gcc ccc 241
284 Ala Lys His Tyr Val Tyr Ile Gly Asp Pro Ala Gln Leu Pro Ala Pro
285 65           70           75           80
287 cgc aca ttg ctg act aaa ggc aca cta gaa cca gaa tat ttt aat tca 289
288 Arg Thr Leu Leu Thr Lys Gly Thr Leu Glu Pro Glu Tyr Phe Asn Ser
289           85           90           95
291 gtg tgc aga ctt atg aaa aca ata ggt cca gac atg ttc ctt gga act 337
292 Val Cys Arg Leu Met Lys Thr Ile Gly Pro Asp Met Phe Leu Gly Thr
293           100           105           110
295 tgt cgc cgt tgt cct gct gaa att gtt gac act gtg agt gct tta gtt 385
296 Cys Arg Arg Cys Pro Ala Glu Ile Val Asp Thr Val Ser Ala Leu Val
297           115           120           125
299 tat gac aat aag cta aaa gca cac aag gag aag tca gct caa tgc ttc 433
300 Tyr Asp Asn Lys Leu Lys Ala His Lys Glu Lys Ser Ala Gln Cys Phe
301           130           135           140
303 aaa atg ttc tac aaa ggt gtt att aca cat gat gtt tca tct gca atc 481
304 Lys Met Phe Tyr Lys Gly Val Ile Thr His Asp Val Ser Ser Ala Ile
305 145           150           155           160
307 aac aga cct caa ata ggc gtt gta aga gaa ttt ctt aca cgc aat cct 529
308 Asn Arg Pro Gln Ile Gly Val Val Arg Glu Phe Leu Thr Arg Asn Pro
309           165           170           175
311 gct tgg aga aaa gct gtt ttt atc tca cct tat aat tca cag aac gct 577
312 Ala Trp Arg Lys Ala Val Phe Ile Ser Pro Tyr Asn Ser Gln Asn Ala
313           180           185           190
315 gta gct tca aaa atc tta gga ttg cct acg cag act gtt gat tca tca 625
316 Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val Asp Ser Ser
317           195           200           205
319 cag ggt tct gaa tat gac tat gtc ata ttc aca caa act act gaa aca 673
320 Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln Thr Thr Glu Thr
321           210           215           220
323 gca cac tct tgt aat gtc aac cgc ttc aat gtg gct atc aca agg gca 721
324 Ala His Ser Cys Asn Val Asn Arg Phe Asn Val Ala Ile Thr Arg Ala
325 225           230           235           240
327 aaa att ggc att ttg tgc ata atg tct gat aga gat ctt tat gac aaa 769
328 Lys Ile Gly Ile Leu Cys Ile Met Ser Asp Arg Asp Leu Tyr Asp Lys

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/06/2004
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Input Set : D:\V9661069.app
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 21,22,23,24,25,26,27

VERIFICATION SUMMARY

DATE: 08/06/2004

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TIME: 14:27:48

Input Set : D:\V9661069.app

Output Set: N:\CRF4\08062004\J808121A.raw

L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0